7D6
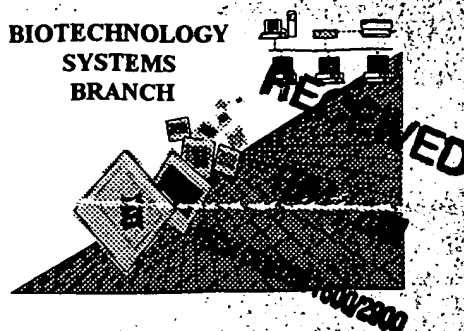
RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/375,924ß_

Source: _1644_

Date Processed by STIC: _2/5/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED   SUGGESTED CORRECTION

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1644

RAW SEQUENCE LISTING   DATE: 02/05/2001
PATENT APPLICATION: US/09/375,924B   TIME: 14:51:42

Input Set : A:\abgx-2 cip.ST25.txt
Output Set: N:\CRF3\02052001\I375924B.raw

p. 2 (handwritten)

Does Not Comply
Corrected Diskette Needed

many of the same (handwritten)
errors as previous (handwritten)
submission (handwritten)

```
 3 <110> APPLICANT: Gallo, Michael
 4         Foord, Orit
 5         Junghans, Richard
 7 <120> TITLE OF INVENTION: GENERATION OF MODIFIED MOLECULES WITH INCREASED SERUM HALF-LIVES
 9 <130> FILE REFERENCE: ABGX-2 CIP
11 <140> CURRENT APPLICATION NUMBER: US 09/375,924B
12 <141> CURRENT FILING DATE: 1999-08-17
14 <150> PRIOR APPLICATION NUMBER: US 60/096,868
15 <151> PRIOR FILING DATE: 1998-08-17
17 <160> NUMBER OF SEQ ID NOS: 10
19 <170> SOFTWARE: PatentIn version 3.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 16
23 <212> TYPE: PRT
24 <213> ORGANISM: homo sapiens
26 <400> SEQUENCE: 1
28 Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr His Thr Cys Pro Pro
29 1               5                   10                  15
31 <210> SEQ ID NO: 2
32 <211> LENGTH: 16
33 <212> TYPE: PRT
34 <213> ORGANISM: Artificial Sequence
36 <220> FEATURE:
37 <221> NAME/KEY: misc_feature
38 <222> LOCATION: ()..()
39 <223> OTHER INFORMATION: modified from human IgG1 hinge region
42 <400> SEQUENCE: 2
44 Ala Glu Pro Lys Ser Ser Asp Lys Thr His Thr His Thr Cys Pro Pro
45 1               5                   10                  15
47 <210> SEQ ID NO: 3
48 <211> LENGTH: 12
49 <212> TYPE: PRT
50 <213> ORGANISM: Homo sapiens
52 <400> SEQUENCE: 3
54 Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro
55 1                5                   10
57 <210> SEQ ID NO: 4
58 <211> LENGTH: 12
59 <212> TYPE: PRT
60 <213> ORGANISM: Homo sapiens
62 <400> SEQUENCE: 4
64 Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro
65 1               5                   10
67 <210> SEQ ID NO: 5
68 <211> LENGTH: 12
69 <212> TYPE: DNA
70 <213> ORGANISM: Homo sapiens
```

RAW SEQUENCE LISTING   DATE: 02/05/2001
PATENT APPLICATION: US/09/375,924B   TIME: 14:51:42

Input Set : A:\abgx-2 cip.ST25.txt
Output Set: N:\CRF3\02052001\I375924B.raw

```
 72 <400> SEQUENCE: 5
 73 tctctgggta aa                                        12
 76 <210> SEQ ID NO: 6
 77 <211> LENGTH: 12
 78 <212> TYPE: DNA
 79 <213> ORGANISM: Artificial/Unknown
 81 <220> FEATURE:
 82 <221> NAME/KEY: misc_feature
 83 <222> LOCATION: ()..()
 84 <223> OTHER INFORMATION: modified sequence
 87 <400> SEQUENCE: 6
 88 tccttaggga ag                                        12
 91 <210> SEQ ID NO: 7
 92 <211> LENGTH: 22
 93 <212> TYPE: DNA
 94 <213> ORGANISM: Artificial/Unknown
 96 <220> FEATURE:
 97 <221> NAME/KEY: misc_feature
 98 <222> LOCATION: ()..()
 99 <223> OTHER INFORMATION: primer 1
102 <400> SEQUENCE: 7
103 gggacccacg gggtgcgagg gc                             22
106 <210> SEQ ID NO: 8
107 <211> LENGTH: 36
108 <212> TYPE: DNA
109 <213> ORGANISM: Artificial/Unknown
111 <220> FEATURE:
112 <221> NAME/KEY: misc_feature
113 <222> LOCATION: ()..()
114 <223> OTHER INFORMATION: primer 2
117 <400> SEQUENCE: 8
118 cttccctaag gacatggaga ggctcttctg tgtgtg              36
121 <210> SEQ ID NO: 9
122 <211> LENGTH: 36
123 <212> TYPE: DNA
124 <213> ORGANISM: Artificial/Unknown
126 <220> FEATURE:
127 <221> NAME/KEY: misc_feature
128 <222> LOCATION: ()..()
129 <223> OTHER INFORMATION: primer 3
132 <400> SEQUENCE: 9
133 gattccttag ggaaggcaga gcccaaatct agtgac              36
136 <210> SEQ ID NO: 10
137 <211> LENGTH: 34
138 <212> TYPE: DNA
139 <213> ORGANISM: Artificial/Unknown
141 <220> FEATURE:
142 <221> NAME/KEY: misc_feature
143 <222> LOCATION: ()..()
```

invalid response - per 1.823 of new Sequence Rules, the only valid <213> responses are: Unknown or Artificial Sequence or Scientific name (Genus/species) one of the three (see circled portion of item 12 on Error Summary Sheet)

144 <223> OTHER INFORMATION: primer 4
147 <400> SEQUENCE: 10
148 gccggaattc ggtacgtgcc aagcatcctc gtgc   34

```
VERIFICATION SUMMARY                DATE: 02/05/2001
PATENT APPLICATION:  US/09/375,924B     TIME: 14:51:43

Input Set : A:\abgx-2 cip.ST25.txt
Output Set: N:\CRF3\02052001\I375924B.raw
```